

cRedAnno+: Annotation Exploitation in Self-Explanatory Lung Nodule Diagnosis

( +)

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(considerably) Reducing Annotation Need in Self-Explanatory Models for Lung Nodule Diagnosis

(cRedAnno 

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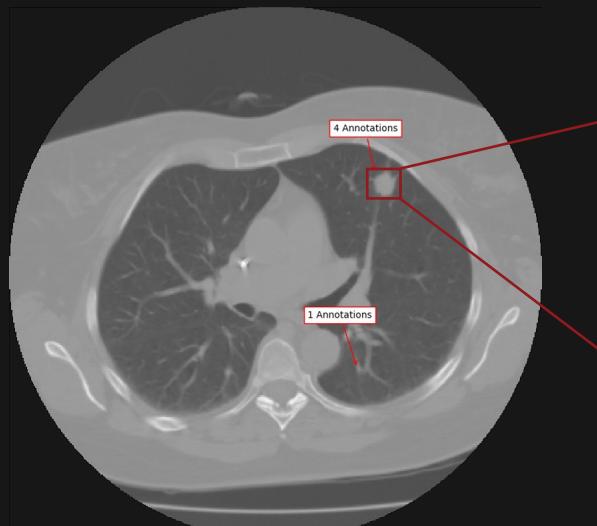


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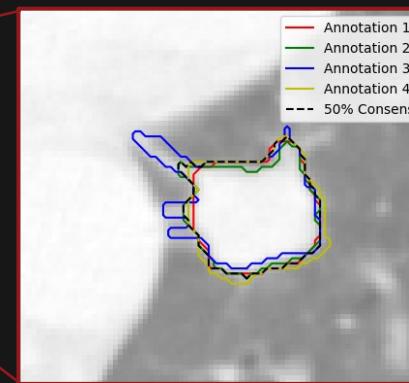
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Background: Lung nodule diagnosis



CT scan

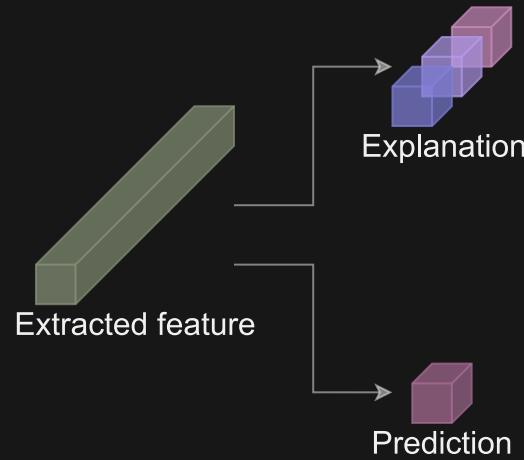
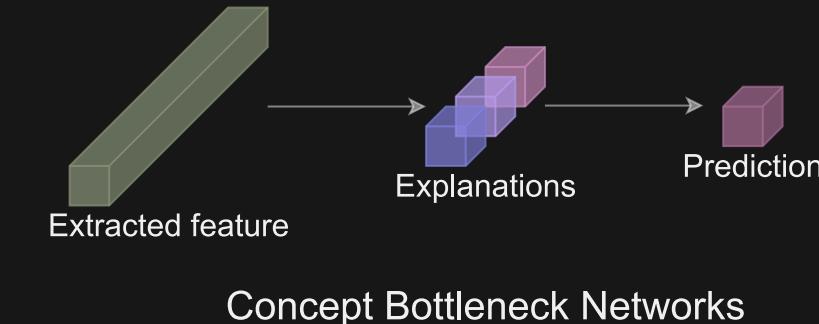
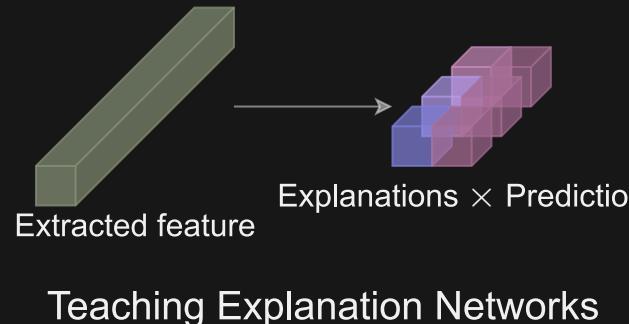


Nodule detection

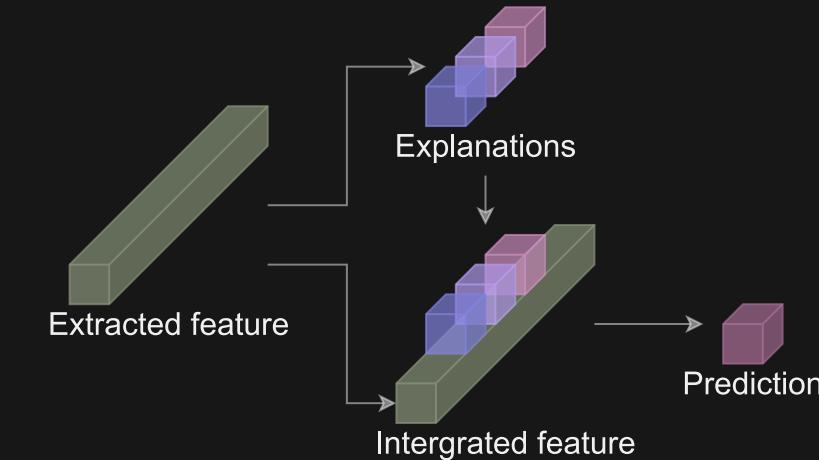
Nodule attributes	
Subtlety	Obvious
InternalStructure	Soft Tissue
Calcification	Non-central
Sphericity	Ovoid
Margin	Sharp
Lobulation	Nearly No Lobulation
Spiculation	Medium Spiculation
Texture	Solid
Malignancy	
Moderately Suspicious	

Annotation info

Related work: Feature-based self-explanatory models

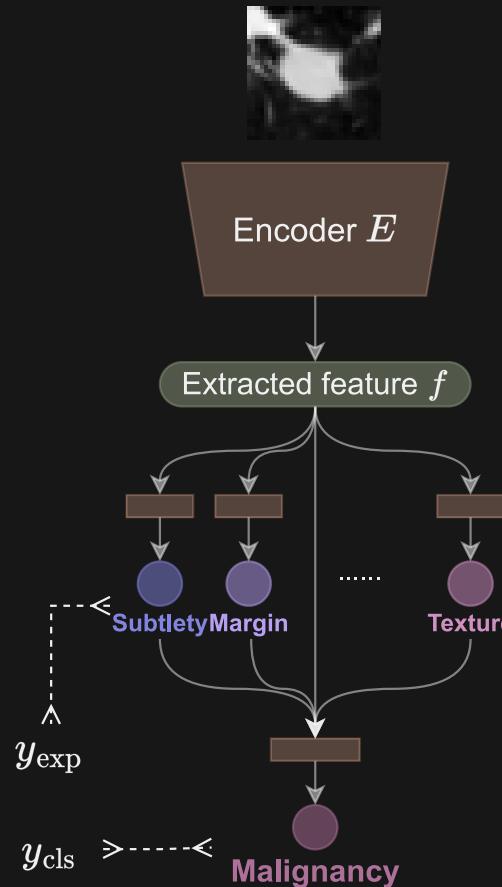


Multitask Learning Networks

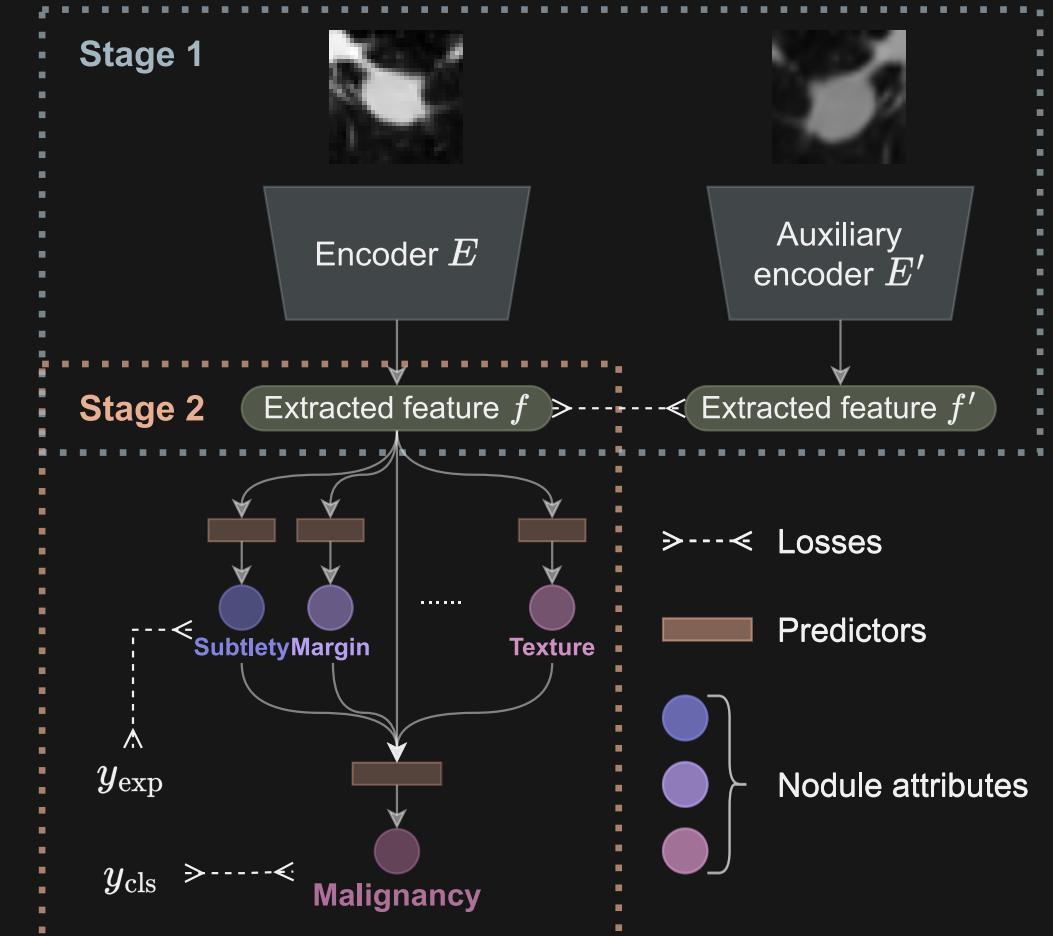


Hierarchical Networks

Method – cRedAnno 🖐: Self-supervised contrastive learning



Previous methods

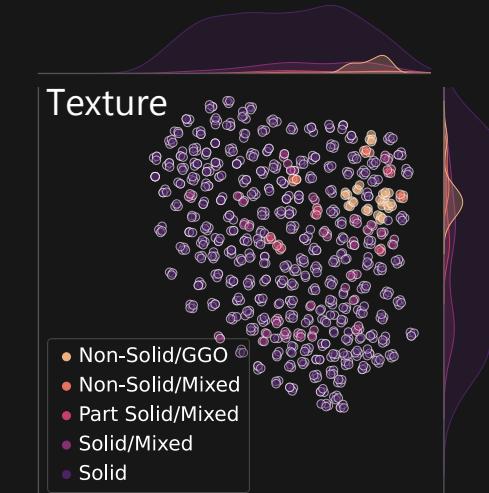
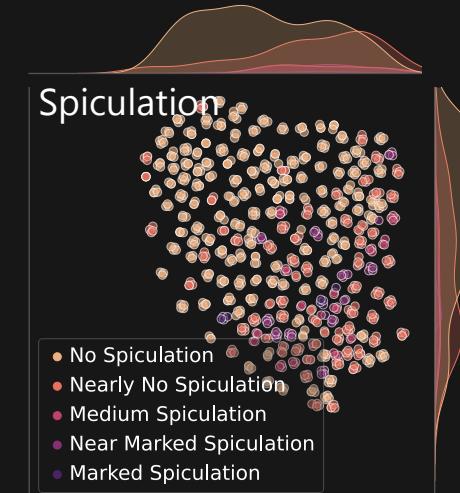
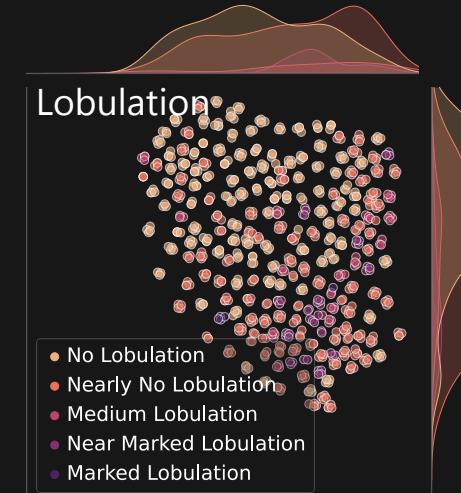
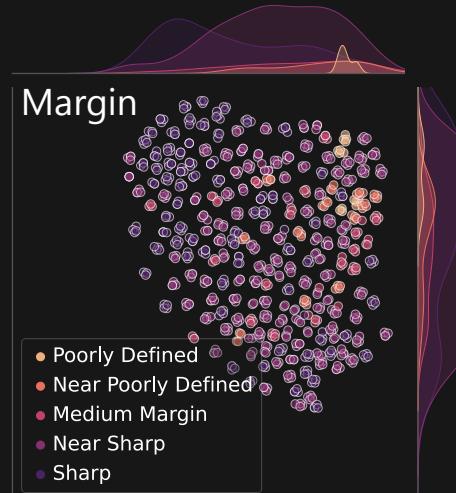
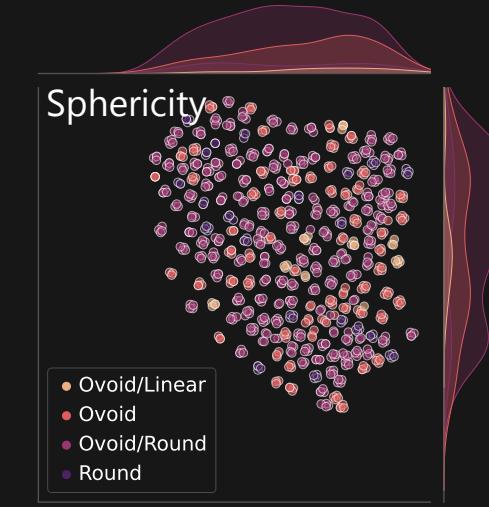
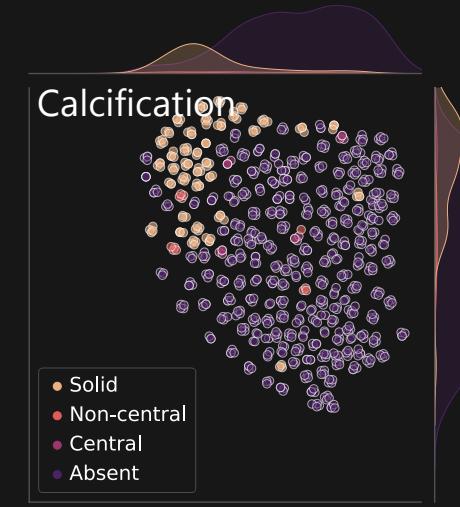
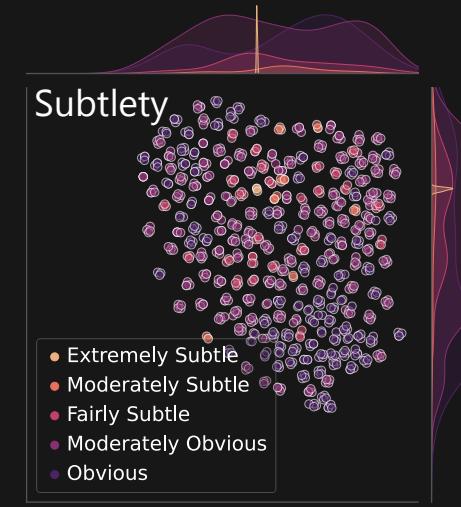
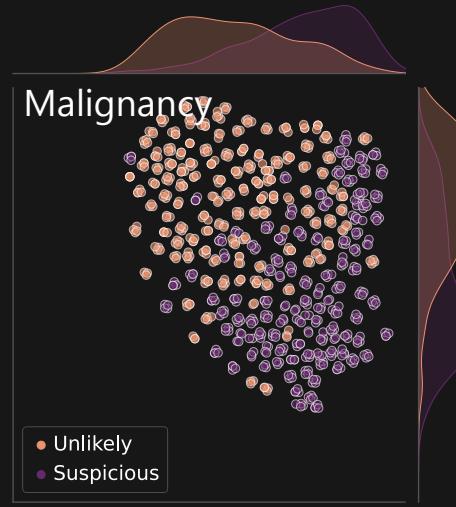


cRedAnno 🖐

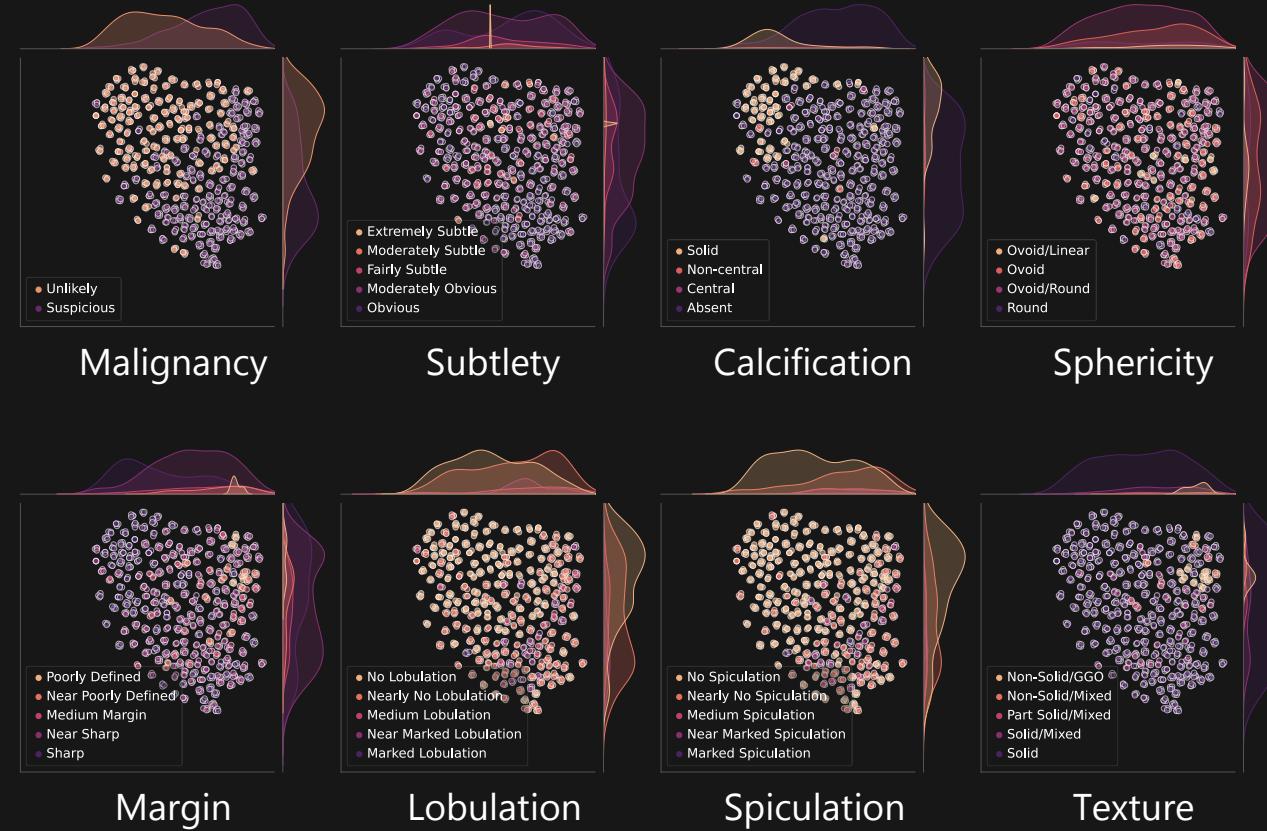
- >---< Losses
- Predictors
- { Nodule attributes

Results:

Analysis of extracted features in the learned space



Limitations of cRedAnno



- Under scarce annotation conditions
 - Unstable performance
- Randomly selected annotations are not necessarily informative enough
 - Risk of not covering enough label space
- Unlabelled data are not adequately used

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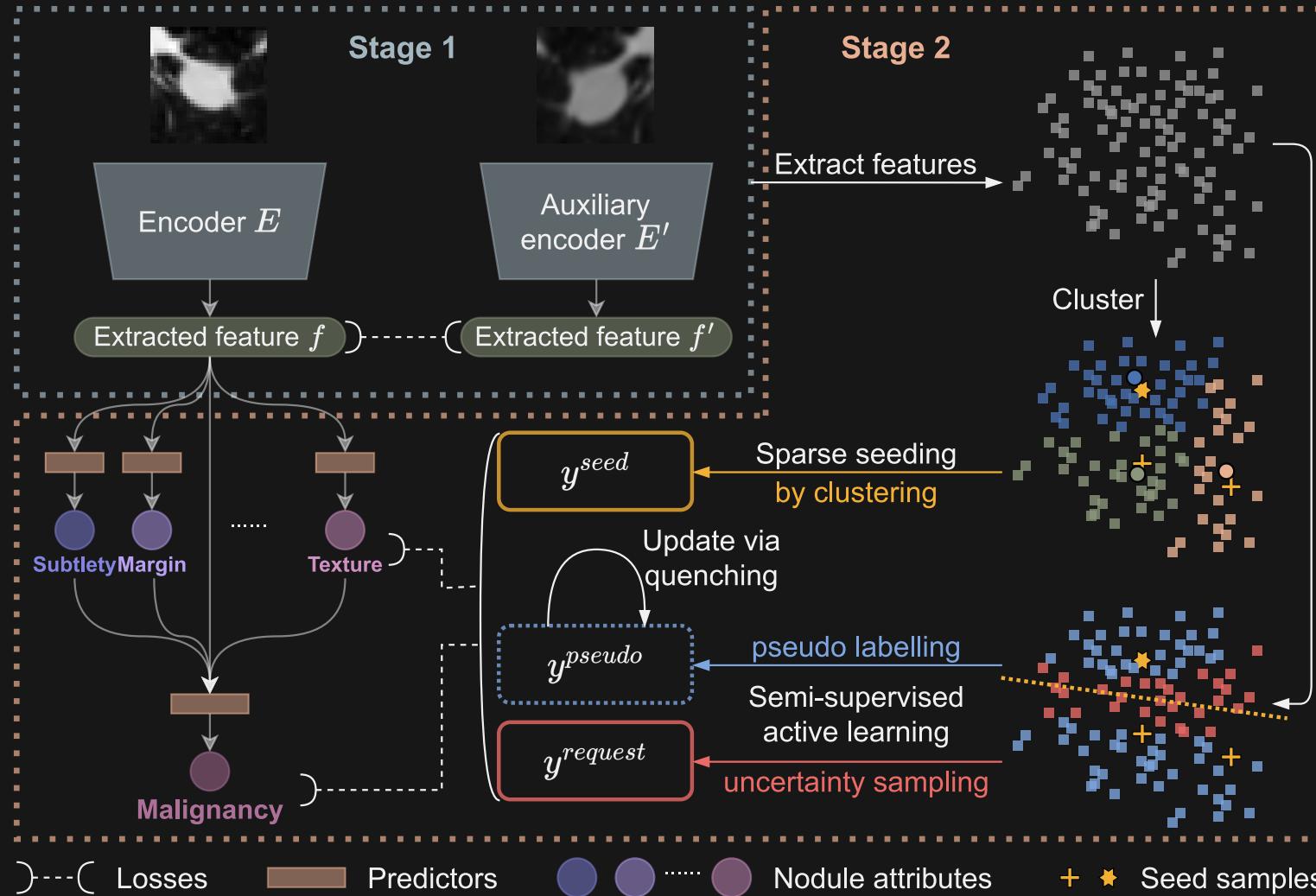


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Method – cRedAnno+ +: Annotation exploitation mechanism



- Aim: jointly utilise
 - extracted features
 - annotations
 - unlabelled data
- Sparse seeding.
 - cluster centroids
- Semi-supervised active learning.
 - uncertainty sampling
 - pseudo labelling
- Quenching.
 - update pseudo labels
 - reinitialise the weights

Results:

Predicting nodule attributes and malignancy

	Nodule attributes							Malignancy	#nODULES	Additional information
	Sub	Cal	Sph	Mar	Lob	Spi	Tex			
Full annotation										
HSCNN ^[1]	71.90	90.80	55.20	72.50	-	-	83.40	84.20	4252	3D volume data
X-Caps ^[2]	90.39	-	85.44	84.14	70.69	75.23	93.10	86.39	1149	None
MSN-JCN ^[3]	70.77	94.07	68.63	78.88	94.75	93.75	89.00	87.07	2616	segmentation mask + ...
MTMR ^[4]	-	-	-	-	-	-	-	93.50	1422	all 2D slices in 3D volumes
+	96.32 ± 0.61	95.88 ± 0.15	97.23 ± 0.20	96.23 ± 0.23	93.93 ± 0.87	94.06 ± 0.60	97.01 ± 0.26	87.56 ± 0.61	730	None
Partial annotation										
WeakSup ^[5] (1:5)	43.10	63.90	42.40	58.50	40.60	38.70	51.20	82.40	2558	multi-scale 3D volume data, all malignancy annotations, 1/(1+N) on attributes
WeakSup ^[5] (1:3)	66.80	91.50	66.40	79.60	74.30	81.40	82.20	89.10		
	96.06 ± 2.02	93.76 ± 0.85	95.97 ± 0.69	94.37 ± 0.79	93.06 ± 0.27	93.15 ± 0.33	95.49 ± 0.85	86.65 ± 1.39	730	None
+ (10%)	96.23 ± 0.45	92.72 ± 1.66	95.71 ± 0.47	90.03 ± 3.68	93.89 ± 1.41	93.67 ± 0.64	92.41 ± 1.05	87.86 ± 1.99		
	93.98 ± 2.09	89.68 ± 3.52	94.02 ± 2.30	91.94 ± 1.17	91.03 ± 1.72	90.81 ± 1.56	93.63 ± 0.47	80.02 ± 8.56		
+ (1%)	95.84 ± 0.34	92.67 ± 1.24	95.97 ± 0.45	91.03 ± 4.65	93.54 ± 0.87	92.72 ± 1.19	92.67 ± 1.50	86.22 ± 2.51		

[1] S. Shen *et al.*, "An interpretable deep hierarchical semantic convolutional neural network for lung nodule malignancy classification," *Expert Systems with Applications*, vol. 128, pp. 84–95, Aug. 2019.

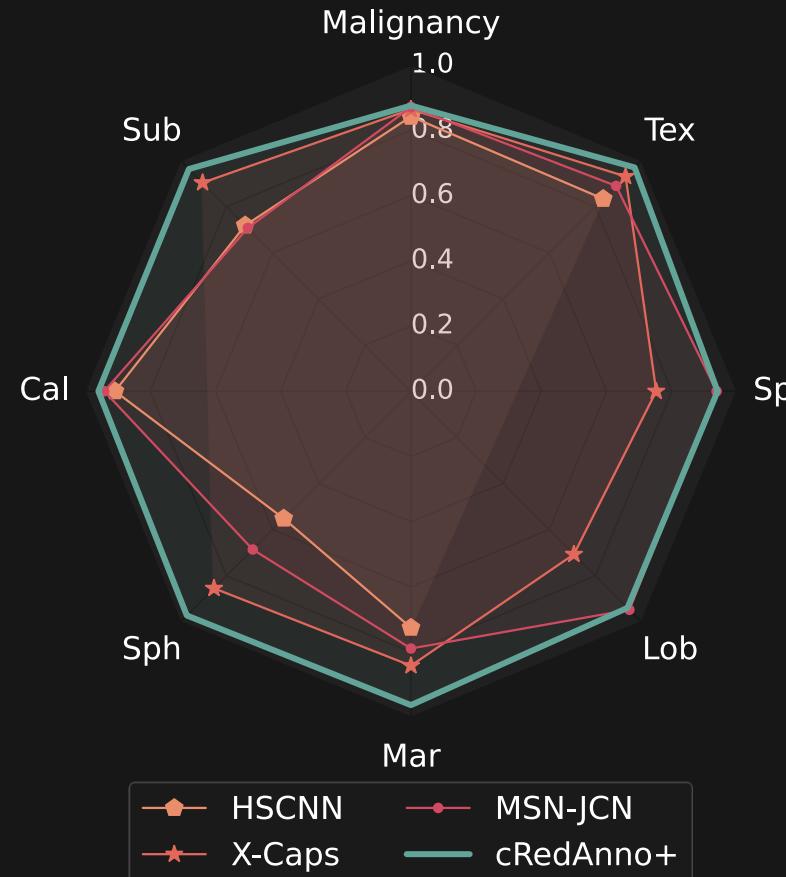
[2] R. LaLonde *et al.*, "Encoding Visual Attributes in Capsules for Explainable Medical Diagnoses," in *Medical Image Computing and Computer Assisted Intervention – MICCAI 2020*, Cham, 2020, pp. 294–304.

[3] W. Chen *et al.*, "End-to-End Multi-Task Learning for Lung Nodule Segmentation and Diagnosis," in *2020 25th International Conference on Pattern Recognition (ICPR)*, Milan, Italy, 2021, pp. 6710–6717.

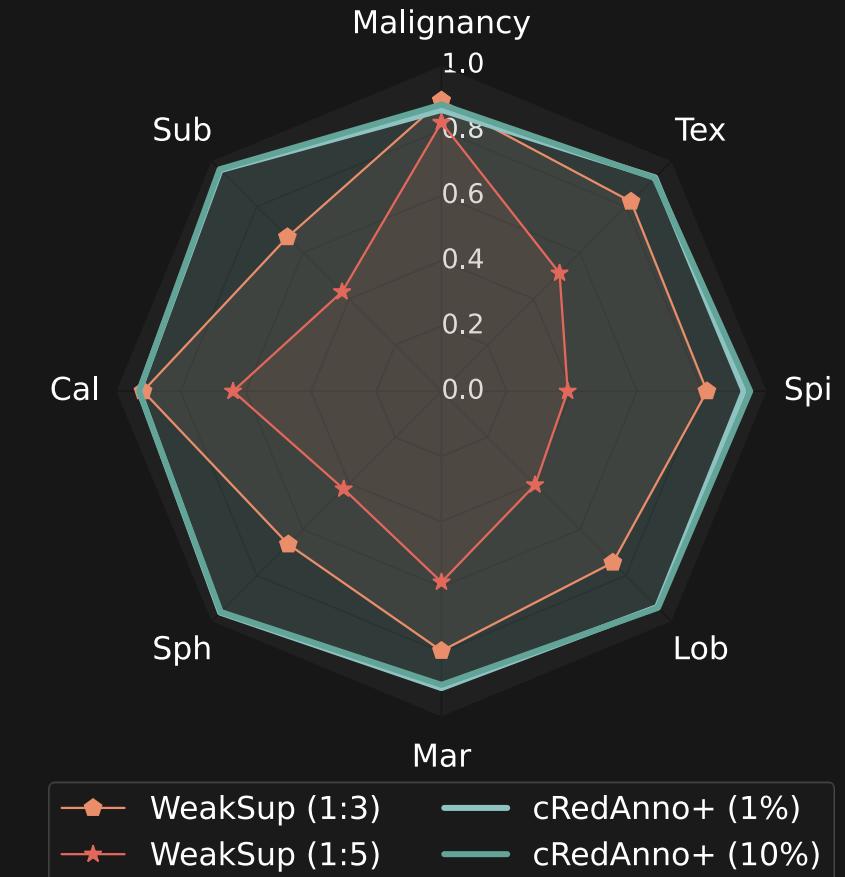
[4] L. Liu *et al.*, "Multi-Task Deep Model With Margin Ranking Loss for Lung Nodule Analysis," *IEEE Trans. Med. Imaging*, vol. 39, no. 3, pp. 718–728, Mar. 2020.

[5] A. Joshi *et al.*, "Lung nodule malignancy classification with weakly supervised explanation generation," *J. Med. Imag.*, vol. 8, no. 04, Aug. 2021.

Results: Predicting nodule attributes and malignancy



Full annotation

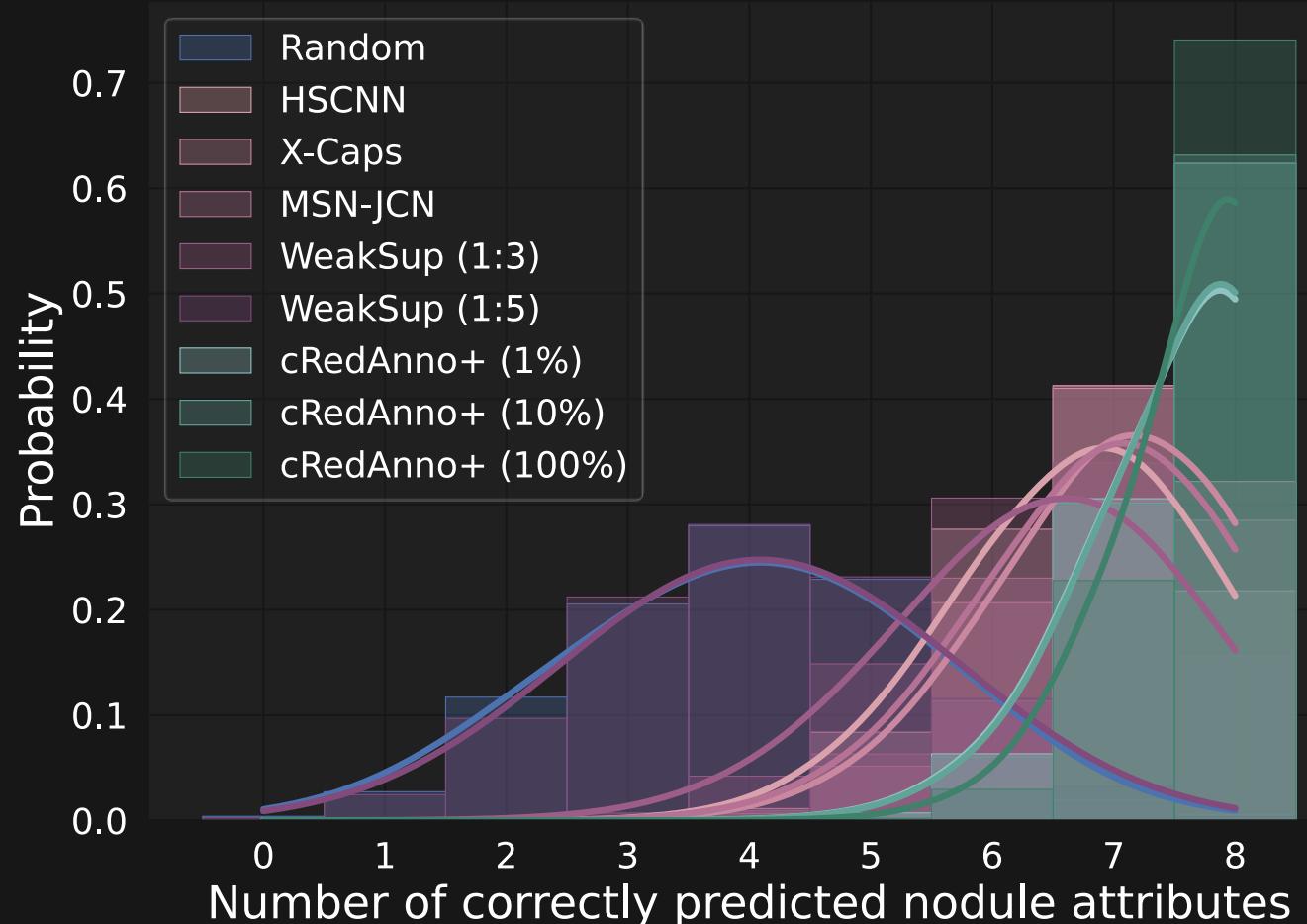


Partial annotation

Simultaneously high accuracy in predicting malignancy and all nodule attributes.

Results:

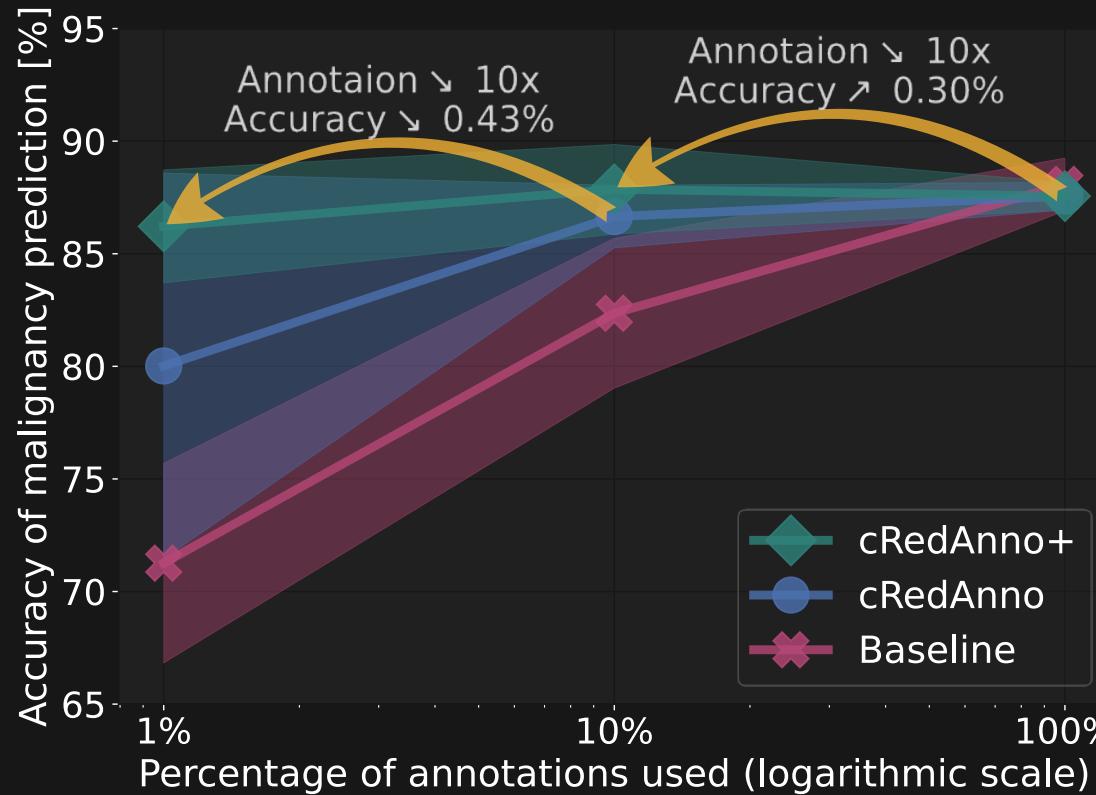
Predicting nodule attributes for a given sample



- cRedAnno+ shows a significantly larger probability of simultaneously predicting all 8 nodule attributes correctly.
- >90% nodules have at least 7 attributes correctly predicted, even under the extreme 1% annotation condition.

Results

Comparison with cRedAnno



Ablation study

Seed sample selection	Annotation acquisition strategy	Pseudo labelling	Quenching	Malignancy accuracy (10%)	Malignancy accuracy (1%)*
random	×	×	×	86.65 ± 1.39	80.02 ± 8.56
random	malignancy confidence	dynamic	✓	82.71 ± 7.47	79.50 ± 11.10
sparse	integrated entropy	dynamic	✓	86.52 ± 0.99	86.22 ± 2.51
sparse	malignancy confidence	static	×	85.91 ± 1.66	85.35 ± 1.93
sparse	malignancy confidence	dynamic	✓	87.86 ± 1.99	86.22 ± 2.51

* Does not contain requested annotations.

Conclusion

- A data-/annotation-efficient self-explanatory approach for lung nodule diagnosis
 - Contrastive learning (☛)
 - learn semantically meaningful reasoning space
 - Annotation exploitation mechanism (☛ +)
 - jointly utilise the extracted features, annotations, and unlabelled data
- Comparing with SOTA:
 - 1% annotation, fewer samples
 - competitive in malignancy prediction
 - significantly better in predicting all nodule attributes as explanations

- Open-source code



github.com/diku-dk/credanno

- Implementation
- Sample selection
- Pre-processing
- Experiments
- Plots

Considerably Reducing Annotation Need in Self-Explanatory Models for Lung Nodule Diagnosis (cRedAnno) and (cRedAnno+)



github.com/diku-dk/credanno

